IN THE SPECIFICATION:

Please amend the paragraph beginning at page 3, line 10, as follows:

--Notwithstanding such complexities, numerous genome sequence efforts designed to determine the exact sequence of the nucleotides found in genomic DNA of various organisms are underway and significant progress has been made. For example, the Human Genome Project began with the specific goal of obtaining the complete sequence of the human genome and determining the biochemical function(s) of each gene. To date, the project has resulted in sequencing a substantial portion of the human genome (J. Roach, on the world wide web at ~~http://~~weber.u.washington.edu/.about.roach/human_genome- _progress2.html) (Gibbs, 1995), and is on track for its scheduled completion in the near future. At least twenty-one other genomes have already been sequenced, including, for example, *M. genitalium* (Fraser et al., 1995), *M. jannaschii* (Bult et al., 1996), *H. influenzae* (Fleischmann et al., 1995), *E. coli* (Blattner et al., 1997), and yeast (*S. cerevisiae*) (Mewes et al., 1997). Significant progress has also been made in sequencing the genomes of model organisms, such as mouse, *C. elegans*, and *D. melanogaster*. Several databases containing genomic information annotated with some functional information are maintained by different organizations, and are accessible via the internet, for example, on the world wide web (www) at ~~http://www.~~tigr.org/tdb; ~~http://www.~~genetics.wisc.edu; ~~http://~~genome-www.stanford.edu/.about.ball; ~~http://~~hiv-web.lanl.gov; ~~http://www.~~ncbi.nlm.nih.gov; ~~http://www.~~ebi.ac.uk; ~~http://~~pasteur.fr/other/biology; and, ~~http://www~~genome.wi.mit.edu. --

Please amend the paragraph beginning at page 4, line 9, as follows:

--To maximize the utility of such nucleotide sequence information, it must be interpreted. Various tools have been developed to assist in this process. For example, algorithms have been developed to analyze what a particular nucleotide sequence encodes, e.g., a regulatory region, an open reading frame (ORF), particularly for protein sequences, or a non-translated RNA, based on homology with known sequences (which are presumed to have similar structures and related

functions). See, e.g., "Frames" (Genetics Computer Group, Madison, Wis.; e.g., on the world wide web at ~~www.~~gcg.com), which is used for identifying ORFs. For sequences predicted or determined to be ORFs, it is possible to determine the amino acid sequence of the protein encoded thereby using simple analytical tools well known in the art. For example, see "Translate" (Genetics Computer Group, Madison, Wis.; e.g., on the world wide web (www) at ~~www.~~gcg.com). However, to date determination of the primary structure of a protein in and of itself provides little, if any, functional information about the protein or its corresponding gene. Thus, the ability to predict the three-dimensional structure of a protein from its amino acid sequence is of great theoretical.sup.1,2 and practical importance.[3] --

Please amend the paragraph beginning at page 52, line 20, as follows:

--As indicated above, FSDs can be built for any type of protein function. Functions of particular interest include enzymatic activities. At present, more than 180 different enzymatic activities have been classified, and are listed by enzyme name in the following table. The particular classification of an enzyme listed in the following table is defined in accordance with the enzyme classification system as described in, e.g., Enzyme Nomenclature, NC-IUBMB, Academic Press, New York, N.Y. (1992), and at ~~www.biochem.ucl.ac.uk/bsm/enzymes/index.html~~ on the world wide web (www) at biochem.ucl.ac.uk/bsm/enzymes/index.html.--